

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Gregory Plowman
Bahija Jallal

(ii) TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
PTP RELATED DISORDERS

(iii) NUMBER OF SEQUENCES: 23

(iv) CORRESPONDENCE ADDRESS:
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Suite 4700
(C) CITY: Los Angeles
(D) STATE: California
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(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: IBM P.C. DOS 5.0
(D) SOFTWARE: FastSEQ for Windows 2.0

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Herewith
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 60/049,756
(B) FILING DATE: June 11, 1997

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:
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(B) REGISTRATION NUMBER: 32,327
(C) REFERENCE/DOCKET NUMBER: 235/054

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	1785 base pairs
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGTTATGTCT	GACTCACTGC	ACTGGAGTTT	GGCAAAAGCA	TCTCAGAAGT	GGTTGTGCTT	60
TTTGATGA	AATGATCAAT	GGAGGTGCTCC	AGTTGTATGC	TGGCCTCTGG	ATACTAACTA	120
GACCTGCCCTG	ACTCCAGGAA	CTAAGGCTCA	GTATCTGCAG	AAGCTTTTG	CCCATCTCAT	180
TCCGGCTATG	GGGACAACAT	GTCTTCACCC	AGGAAGGTTA	GAGGAAAAC	TGGAAGAGAT	240
AATGATGAAG	AGGAGGGTAA	TTCAGGTAAC	CTGAATCTCC	GCAACTCTTT	GCCTTCATCG	300
AGTCAGAAAA	TGACGCCTAC	GAAGCCGATT	TTTGGGAATA	AAATGAATTTC	AGAGAATGTA	360
AAACCCCTCCC	ATCACCTGTC	ATTCTCAGAT	AAGTATGAGC	TTGTTTACCC	AGAGCCTTTG	420
GAAAGTGACA	CTGATGAGAC	TGTGTTGGAT	GTCAGTGAAC	GGTCTCTCAG	AAACAGGTGG	480
AACAGTATGG	ATTCAGAGAC	TGCAGGGCCG	TCAAAGACTG	TCTCCCCAGT	GCTTTCTGGT	540
AGTAGTAGGC	TCTCAAAGGA	CACTGAAACA	TCTGTCTCTG	AAAAGGAGCT	AACTCAGTTG	600
GCTCAGATTC	GACCATTAAAT	ATTCAACAGT	TCTGCACGGT	CTGCTATGCG	GGATTGTTTG	660
AACACGCTTC	AGAAAAAAGA	AGAACTTGAT	ATCATCCGTG	AGTTTTGGA	TTAGAACAA	720
ATGACTCTGC	CTGATGACTT	CAATTCTGGG	AATACACTAC	AGAACAGAGA	TAAGAACAGA	780
TACCGAGATA	TTCTTCCATA	TGATTCAACA	CGTGTTCCTC	TTGGAAAAAA	CAAGGACTAC	840
ATCAACGCTA	GTTATATTAG	AATAGTAAT	CATGAAGAAG	AGTATTTTA	TATTGCCACT	900
CAAGGACCAT	TGCCAGAAC	TATAGAAGAC	TTTGGCAAA	TGGTTCTGGA	AAAAATTGT	960
AATGTTATTG	CTATGATAAC	CAGAGAGATA	GAATGTGGAG	TTATCAAGT	TTACAGTTAC	1020
TGGCCCATTT	CTCTGAAGGA	GCCTTTGGAA	TTCGAACACT	TTAGTGTCTT	TCTGGAGACC	1080
TTTCATGTAA	CTCAATATT	CACCGTTCGA	GTATTTCAGA	TTGTGAAGAA	GTCCACAGGA	1140
AAGAGCCAAT	GTGTAAAACA	CTTGCACTTC	ACCAAGTGGC	CAGACCATGG	CACTCCTGCC	1200
TCAGCAGATT	TTTCATAAA	ATATGTCCGT	TATGTGAGGA	AGGCCACAT	TACAGGACCC	1260
CTCCTTGTTC	ACTGCAGTGC	TGGTGTAGGC	CGAACAGGGG	TGTTCATATG	TGTGGATGTT	1320
GTGTTCTCTG	CCATCGAGAA	GAACTAACCT	TTTGACATTA	TGAACATAGT	GACCCAGATG	1380
AGAAAGCAGC	GCTGTGGCAT	GATTCAAACC	AAGGAGCAGT	ACCAGTTTG	TTATGAAATT	1440
GTGCTTGAAG	TTCTTCAGAA	CCTTCTGGCT	TTGTATTAAG	AGAGACTTCT	GCGCCTGTCC	1500
CTCGAGGTAA	CCGAGCAGCT	TGGAGCTGA	GCCGTGCTGA	AGCGTCTGCG	GGCGCTGCA	1560
TCTGCCCTCT	GATTTTCTC	TCTGAAAGTC	CCTGAAGGTA	GCACTACTGG	GCACAGAGTG	1620
AACTGTTTCC	ACTTGATCTT	TCTGAACAAAG	AGCAAAATAC	CCTCCATGCC	TTCTACGGAA	1680
ACGGAAGTTG	CATGAAACAA	CCTCCGCTTG	GCTGTCTGGT	TTGTGGTATT	ACAGAGCTTA	1740
ATAAAAGACT	TAGATGTGAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAA		1785

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	1896 base pairs
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGTTATGTCT	GACTCACTGC	ACTGGAGTTT	GGCAAAAGCA	TCTCAGAAGT	GGTTGTGCTT
------------	------------	------------	------------	------------	------------

60

TTTTGAATGA	AATGATCAAT	GGAGTGCTCC	AGTTGTATGC	TGGCCTCTGG	ATACTAACTA	120
GACCTGCCG	ACTCCAGGAA	CTAAGGCTCA	GTATCTGCAG	AAGCTTTTG	CCCATCTCAT	180
TCCGGCTATG	GGGACAACAT	GTCTTCACCC	AGGAAGGTTA	GAGGAAAAAC	TGGAAGAGAT	240
AATGATGAAG	AGGAGGGTAA	TTCAGGTAAC	CTGAATCTCC	GCAACTCTT	GCCTTCATCG	300
AGTCAGAAA	TGACGCCTAC	GAAGCCGGTA	CAAAATAAAA	ATCTCATGAA	GTATGAAGAA	360
CACTTAGATA	TATTGATGGT	GTTTTTATTG	ATAAAAACCA	TATGGTATAA	TGTCTTCAAA	420
TTATGGAAAG	GCAAGCTTAT	TTTGGGAAT	AAAATGAATT	CAGAGAATGT	AAAACCCCTCC	480
CATCACCTGT	CATTCTCAGA	TAAGTATGAG	CTTGTCTTAC	CAGAGCCTT	GGAAAGTGAC	540
ACTGATGAGA	CTGTGTGGG	TGTCAGTGC	CGGTCTCTCA	GAAACAGGTG	GAACAGTATG	600
GATTAGAGA	CTGCAGGGCC	GTCAAAGACT	GTCTCCCCAG	TGCTTCTGG	TAGTAGTAGG	660
CTCTCAAAGG	ACACTGAAAC	ATCTGTCTC	GAAAAGGAGC	TAATCAGTT	GGCTCAGATT	720
CGACCAATTAA	TATTCACACAG	TTCTGCACGG	TCTGCTATGC	GGGATTGTT	AAACACGCTT	780
CAGAAAAAAG	AAGAACTTGA	TATCATCCGT	GAGTTTTTGG	AGTTAGAACAA	AATGACTCTG	840
CCTGATGACT	TCAATTCTGG	GAATACACTA	CAGAACAGAG	ATAAGAACAG	ATACCGAGAT	900
ATTCTTCCAT	ATGATTCAAC	ACGTGTTCC	CTTGGAAAAAA	ACAAGGACTA	CATCAACGCT	960
AGTTATATTA	GAATAGTAAA	TCATGAAGAA	GAGTATTTT	ATATTGCCAC	TCAAGGACCA	1020
TTGCCAGAAA	CTATAGAAGA	CTTTGGCAA	ATGGTTCTGG	AAAATAATTG	TAATGTTATT	1080
GCTATGATAA	CCAGAGAGAT	AGAATGTGGA	GTTATCAAGT	GTTACAGTTA	CTGGCCCAT	1140
TCTCTGAAGG	AGCCTTTGGA	ATTGAAACAC	TTTGTGTCT	TTCTGGAGAC	CTTTCATGTA	1200
ACTCAATATT	TCACCGTTCG	AGTATTTTCAG	ATTGTGAAGA	AGTCCACAGG	AAAGAGCCAA	1260
TGTGTAAAC	ACTTGCAGTT	CACCAAGTGG	CCAGACCATG	GCACCTCTGC	CTCAGCAGAT	1320
TTTTTCATAA	AATATGTCCG	TTATGTGAGG	AAGAGCCACA	TTACAGGACC	CCTCCTTGTT	1380
CACTGCAGTG	CTGGGTGAGG	CCGAACAGGG	GTGTTCATAT	GTGTGGATGT	TGTGTTCTCT	1440
GCCATCGAGA	AGAACTACTC	TTTTGACATT	ATGAACATAG	TGACCCAGAT	GAGAAAGCAG	1500
CGCTGTGGCA	TGATTCAAAC	CAAGGAGCAG	TACCAAGTTT	GTTATGAAAT	TGTGCTTGA	1560
GTTCTTCAGA	ACCTCTGGC	TTTGTATTAA	GAGAGACTTC	TGCGCCTGTC	CCTCGAGGTT	1620
ACCGAGCAGC	TTGGAGCCTG	AGCCGTGCTG	AAGCGTCTGC	GGGCCGTGCA	GTCTGCCTTC	1680
TGATTTTCT	CTCTGAAAGT	CCCTGAAGGT	AGCACTACTG	GGCACAGAGT	GAACTGTTTC	1740
CACTTGATCT	TTCTGAACAA	GAGAAAATA	CCCTCCATGC	CTTCTACGGA	AACGGAAGTT	1800
GCATGAAACA	ACCTCCGCTT	GGCTGTCCTG	TTTGTGGTAT	TACAGAGCTT	AATAAAAGAC	1860
TTAGATGTGA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAA			1896

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1692 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGTTATGTCT	GACTCACTGC	ACTGGAGTTT	GGCAAAAGCA	TCTCAGAACT	GGTTGTGCTT	60
TTTTGAATGA	AATGATCAAT	GGAGTGCTCC	AGTTGTATGC	TGGCCTCTGG	ATACTAACTA	120
GACCTGCCG	ACTCCAGGAA	CTAAGGCTCA	GTATCTGCAG	AAGCTTTTG	CCCATCTCAT	180
TCCGGCTATG	GGGACAACAT	GTCTTCACCC	AGGAAGGTTA	GAGGAAAAAC	TGGAAGAGAT	240
AATGATGAAG	AGGAGGGTAA	TTCAGGTAAC	CTGAATCTCC	GCAACTCTT	GCCTTCATCG	300
AGTCAGAAA	TGACGCCTAC	GAAGCCGATT	TTTGGGAATA	AAATGAATT	AGAGAATGTA	360
AAACCCCTCC	ATCACCTGTC	ATTCTCAGAT	AAGTATGAGC	TTGTTACCC	AGAGCCTTG	420
GAAAGTGACA	CTGATGAGAC	TGTTGGGAT	GTCAGTGCAC	GGTCTCTCAG	AAACAGGTGG	480
AACAGTATGG	ATTCAAGAC	TGCAGGGCCG	TCAAAGACTG	TCTCCCCAGT	GCTTCTGGT	540
AGTAGTAGGC	TCTCAAAGGA	CACTGAAACA	TCTGTCTCTG	AAAAGGAGCT	AACTCAGTTG	600
GCTCAGATTC	GACCAATTAA	ATTCAACAGT	TCTGCACGGT	CTGCTATGCG	GGATTGTTTG	660
AACACGCTC	AGAAAAAAGA	AGAACTTGAT	ATCATCCGTG	AGTTTTGGA	GTAGAACAA	720
ATGACTCTGC	CTGATGACTT	CAATTCTGGG	AATACACTAC	AGAACAGAGA	TAAGAACAGA	780
TACCGAGATA	TTCTTCATA	TGATTCAACA	CGTGTTCCTC	TTGGAAAAAA	CAAGGACTAC	840
ATCAACGCTA	GTTATATTAG	AATAGTAAAT	CATGAAGAAG	AGTATTTTA	TATTGCCACT	900
CAAGGACCAT	TGCCAGAAC	TATAGAAGAC	TTTGGAAA	TGGTTCTGGA	AAATAATTGT	960
AATGTTATTG	CTATGATAAC	CAGAGAGATA	GAATGTGGAG	TTATCAAGTG	TTACAGTTAC	1020

TGGCCCATT	CTCTGAAGGA	GCCTTGAA	TTCGAACACT	TTAGTGTCTT	TCTGGAGACC	1080
TTTCATGAA	CTCAATATT	CACCGTCGA	GTATTCAGA	TTGTGAAGAA	GTCCACAGGA	1140
AAGAGCCAAT	GTGTAAAACA	CTTGCAGTTC	ACCAAGTGGC	CAGACCAGATGG	CACTCCTGCC	1200
TCAGCAGATT	TTTCATAAA	ATATGTCCGT	TATGTGAGGA	AGAGCCACAT	TACAGGACCC	1260
CTCCTTGTTC	ACTGCAGTGC	TGGTGTAGGC	CGAACAGGGG	TGTTCATATG	TGTGGATGTT	1320
GTGTTCTCTG	CCATCGAGAA	GAACTACTCT	TTTGACATTA	TGAACATAGT	GACCCAGATG	1380
AGAAAGCAGC	GCTGTGGCAT	GATTCAAACC	AAGGTTACCG	AGCAGCTTGG	AGCCTGAGCC	1440
GTGCTGAAGC	GTCTGCGGGC	CGTGCAGTCT	GCCTTCTGAT	TTTTCTCTCT	GAAAGTCCCT	1500
GAAGGTAGCA	CTACTGGGCA	CAGAGTGAAC	TGTTTCCACT	TGAATCTTCT	GAACAAGAGC	1560
AAAATACCTC	CCATGCCTTC	TACGGAAACG	GAAGTTGCAT	GAAACAACCT	CCGCTTGGCT	1620
GTCTGGTTG	TGGTATTACAA	GAGCTTAATA	AAAGACTTAG	ATGTGAAAAA	AAAAAAAAAA	1680
	AA					1692

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAAAATAATT	GTAATGTTAT	TGCTATGATA	ACCAAGAGAGA	TAGAAGGTGG	AGTTATCAAG	60
TGTTGCAGTT	ACTGGCCCGT	TTCTCTGAAG	GAGCCTTGG	AATTCAAACA	CTTCATGTC	120
CTTCTGGAGA	ACTTTCAGAT	AACTCAGTAT	TTTGTCAATCC	GAATATTCA	AATTGTGAAG	180
AAGTCCACAG	GAAAGAGTC	CTCTGTAAAA	CACTTGCAGT	TCATCAAATG	GCCAGACCAT	240
GGCACTCCGT	CCTCAGTAGA	TTTTTCATC	AAATATGTCC	GTTATGTGAG	GAAGAGCCAC	300
ATTACAGGAC	CCCTCCTTGT					320

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Ser	Ser	Pro	Arg	Lys	Val	Arg	Gly	Lys	Thr	Gly	Arg	Asp	Asn	Asp
1						5			10				15		
Glu	Glu	Glu	Gly	Asn	Ser	Gly	Asn	Leu	Asn	Leu	Arg	Asn	Ser	Leu	Pro
								20		25		30			
Ser	Ser	Ser	Gln	Lys	Met	Thr	Pro	Thr	Lys	Pro	Ile	Phe	Gly	Asn	Lys
					35			40			45				
Met	Asn	Ser	Glu	Asn	Val	Lys	Pro	Ser	His	His	Leu	Ser	Phe	Ser	Asp
	50					55					60				
Lys	Tyr	Glu	Leu	Val	Tyr	Pro	Glu	Pro	Leu	Glu	Ser	Asp	Thr	Asp	Glu
	65					70				75		80			

Thr Val Trp Asp Val Ser Asp Arg Ser Leu Arg Asn Arg Trp Asn Ser
 85 90 95

Met Asp Ser Glu Thr Ala Gly Pro Ser Lys Thr Val Ser Pro Val Leu
 100 105 110

Ser Gly Ser Ser Arg Leu Ser Lys Asp Thr Glu Thr Ser Val Ser Glu
 115 120 125

Lys Glu Leu Thr Gln Leu Ala Gln Ile Arg Pro Leu Ile Phe Asn Ser
 130 135 140

Ser Ala Arg Ser Ala Met Arg Asp Cys Leu Asn Thr Leu Gln Lys Lys
 145 150 155 160

Glu Glu Leu Asp Ile Ile Arg Glu Phe Leu Glu Leu Glu Gln Met Thr
 165 170 175

Leu Pro Asp Asp Phe Asn Ser Gly Asn Thr Leu Gln Asn Arg Asp Lys
 180 185 190

Asn Arg Tyr Arg Asp Ile Leu Pro Tyr Asp Ser Thr Arg Val Pro Leu
 195 200 205

Gly Lys Asn Lys Asp Tyr Ile Asn Ala Ser Tyr Ile Arg Ile Val Asn
 210 215 220

His Glu Glu Glu Tyr Phe Tyr Ile Ala Thr Gln Gly Pro Leu Pro Glu
 225 230 235 240

Thr Ile Glu Asp Phe Trp Gln Met Val Leu Glu Asn Asn Cys Asn Val
 245 250 255

Ile Ala Met Ile Thr Arg Glu Ile Glu Cys Gly Val Ile Lys Cys Tyr
 260 265 270

Ser Tyr Trp Pro Ile Ser Leu Lys Glu Pro Leu Glu Phe Glu His Phe
 275 280 285

Ser Val Phe Leu Glu Thr Phe His Val Thr Gln Tyr Phe Thr Val Arg
 290 295 300

Val Phe Gln Ile Val Lys Lys Ser Thr Gly Lys Ser Gln Cys Val Lys
 305 310 315 320

His Leu Gln Phe Thr Lys Trp Pro Asp His Gly Thr Pro Ala Ser Ala
 325 330 335

Asp Phe Phe Ile Lys Tyr Val Arg Tyr Val Arg Lys Ser His Ile Thr
 340 345 350

Gly Pro Leu Leu Val His Cys Ser Ala Gly Val Gly Arg Thr Gly Val
 355 360 365

Phe Ile Cys Val Asp Val Val Phe Ser Ala Ile Glu Lys Asn Tyr Ser
 370 375 380

Phe Asp Ile Met Asn Ile Val Thr Gln Met Arg Lys Gln Arg Cys Gly
 385 390 395 400

Met Ile Gln Thr Lys Glu Gln Tyr Gln Phe Cys Tyr Glu Ile Val Leu
 405 410 415

Glu Val Leu Gln Asn Leu Leu Ala Leu Tyr
 420 425

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 463 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ser Ser Pro Arg Lys Val Arg Gly Lys Thr Gly Arg Asp Asn Asp
 1 5 10 15

Glu Glu Glu Gly Asn Ser Gly Asn Leu Asn Leu Arg Asn Ser Leu Pro
 20 25 30

Ser Ser Ser Gln Lys Met Thr Pro Thr Lys Pro Val Gln Asn Lys Asn
 35 40 45

Leu Met Lys Tyr Glu Glu His Leu Asp Ile Leu Met Val Phe Leu Leu
 50 55 60

Ile Lys Thr Ile Trp Tyr Asn Val Phe Lys Leu Trp Lys Gly Lys Leu
 65 70 75 80

Ile Phe Gly Asn Lys Met Asn Ser Glu Asn Val Lys Pro Ser His His
 85 90 95

Leu Ser Phe Ser Asp Lys Tyr Glu Leu Val Tyr Pro Glu Pro Leu Glu
 100 105 110

Ser Asp Thr Asp Glu Thr Val Trp Asp Val Ser Asp Arg Ser Leu Arg
 115 120 125

Asn Arg Trp Asn Ser Met Asp Ser Glu Thr Ala Gly Pro Ser Lys Thr
 130 135 140

Val Ser Pro Val Leu Ser Gly Ser Ser Arg Leu Ser Lys Asp Thr Glu
 145 150 155 160

Thr Ser Val Ser Glu Leu Thr Gln Leu Ala Gln Ile Arg Pro
 165 170 175

Leu Ile Phe Asn Ser Ser Ala Arg Ser Ala Met Arg Asp Cys Leu Asn
 180 185 190

Thr Leu Gln Lys Lys Glu Glu Leu Asp Ile Ile Arg Glu Phe Leu Glu
 195 200 205

Leu Glu Gln Met Thr Leu Pro Asp Asp Phe Asn Ser Gly Asn Thr Leu
 210 215 220

Gln Asn Arg Asp Lys Asn Arg Tyr Arg Asp Ile Leu Pro Tyr Asp Ser
 225 230 235 240

Thr Arg Val Pro Leu Gly Lys Asn Lys Asp Tyr Ile Asn Ala Ser Tyr
 245 250 255
 Ile Arg Ile Val Asn His Glu Glu Glu Tyr Phe Tyr Ile Ala Thr Gln
 260 265 270
 Gly Pro Leu Pro Glu Thr Ile Glu Asp Phe Trp Gln Met Val Leu Glu
 275 280 285
 Asn Asn Cys Asn Val Ile Ala Met Ile Thr Arg Glu Ile Glu Cys Gly
 290 295 300
 Val Ile Lys Cys Tyr Ser Tyr Trp Pro Ile Ser Leu Lys Glu Pro Leu
 305 310 315 320
 Glu Phe Glu His Phe Ser Val Phe Leu Glu Thr Phe His Val Thr Gln
 325 330 335
 Tyr Phe Thr Val Arg Val Phe Gln Ile Val Lys Lys Ser Thr Gly Lys
 340 345 350
 Ser Gln Cys Val Lys His Leu Gln Phe Thr Lys Trp Pro Asp His Gly
 355 360 365
 Thr Pro Ala Ser Ala Asp Phe Phe Ile Lys Tyr Val Arg Tyr Val Arg
 370 375 380
 Lys Ser His Ile Thr Gly Pro Leu Leu Val His Cys Ser Ala Gly Val
 385 390 395 400
 Gly Arg Thr Gly Val Phe Ile Cys Val Asp Val Val Phe Ser Ala Ile
 405 410 415
 Glu Lys Asn Tyr Ser Phe Asp Ile Met Asn Ile Val Thr Gln Met Arg
 420 425 430
 Lys Gln Arg Cys Gly Met Ile Gln Thr Lys Glu Gln Tyr Gln Phe Cys
 435 440 445
 Tyr Glu Ile Val Leu Glu Val Leu Gln Asn Leu Leu Ala Leu Tyr
 450 455 460

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ser Ser Pro Arg Lys Val Arg Gly Lys Thr Gly Arg Asp Asn Asp
 1 5 10 15

Glu Glu Glu Gly Asn Ser Gly Asn Leu Asn Leu Arg Asn Ser Leu Pro
 20 25 30

Ser Ser Ser Gln Lys Met Thr Pro Thr Lys Pro Ile Phe Gly Asn Lys
 35 40 45

Met Asn Ser Glu Asn Val Lys Pro Ser His His Leu Ser Phe Ser Asp
 50 55 60

Lys Tyr Glu Leu Val Tyr Pro Glu Pro Leu Glu Ser Asp Thr Asp Glu
 65 70 75 80

Thr Val Trp Asp Val Ser Asp Arg Ser Leu Arg Asn Arg Trp Asn Ser
 85 90 95

Met Asp Ser Glu Thr Ala Gly Pro Ser Lys Thr Val Ser Pro Val Leu
 100 105 110

Ser Gly Ser Ser Arg Leu Ser Lys Asp Thr Glu Thr Ser Val Ser Glu
 115 120 125

Lys Glu Leu Thr Gln Leu Ala Gln Ile Arg Pro Leu Ile Phe Asn Ser
 130 135 140

Ser Ala Arg Ser Ala Met Arg Asp Cys Leu Asn Thr Leu Gln Lys Lys
 145 150 155 160

Glu Glu Leu Asp Ile Ile Arg Glu Phe Leu Glu Leu Glu Gln Met Thr
 165 170 175

Leu Pro Asp Asp Phe Asn Ser Gly Asn Thr Leu Gln Asn Arg Asp Lys
 180 185 190

Asn Arg Tyr Arg Asp Ile Leu Pro Tyr Asp Ser Thr Arg Val Pro Leu
 195 200 205

Gly Lys Asn Lys Asp Tyr Ile Asn Ala Ser Tyr Ile Arg Ile Val Asn
 210 215 220

His Glu Glu Glu Tyr Phe Tyr Ile Ala Thr Gln Gly Pro Leu Pro Glu
 225 230 235 240

Thr Ile Glu Asp Phe Trp Gln Met Val Leu Glu Asn Asn Cys Asn Val
 245 250 255

Ile Ala Met Ile Thr Arg Glu Ile Glu Cys Gly Val Ile Lys Cys Tyr
 260 265 270

Ser Tyr Trp Pro Ile Ser Leu Lys Glu Pro Leu Glu Phe Glu His Phe
 275 280 285

Ser Val Phe Leu Glu Thr Phe His Val Thr Gln Tyr Phe Thr Val Arg
 290 295 300

Val Phe Gln Ile Val Lys Lys Ser Thr Gly Lys Ser Gln Cys Val Lys
 305 310 315 320

His Leu Gln Phe Thr Lys Trp Pro Asp His Gly Thr Pro Ala Ser Ala
 325 330 335

Asp Phe Phe Ile Lys Tyr Val Arg Tyr Val Arg Lys Ser His Ile Thr
 340 345 350

Gly Pro Leu Leu Val His Cys Ser Ala Gly Val Gly Arg Thr Gly Val
 355 360 365

Phe Ile Cys Val Asp Val Val Phe Ser Ala Ile Glu Lys Asn Tyr Ser
 370 375 380

Phe Asp Ile Met Asn Ile Val Thr Gln Met Arg Lys Gln Arg Cys Gly
 385 390 395 400

Met Ile Gln Thr Lys
 405

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asp Phe Trp Gly Met Met Trp Glu Asn Asn Cys Asn Val Ile Ala Met
 1 5 10 15

Ile Thr Arg Glu Ile Glu Gly Gly Val Ile Lys Cys Cys Ser Tyr Trp
 20 25 30

Pro Val Ser Leu Lys Glu Pro Leu Glu Phe Lys His Phe His Val Leu
 35 40 45

Leu Glu Asn Phe Gln Ile Thr Gln Tyr Phe Val Ile Arg Ile Phe Gln
 50 55 60

Ile Val Lys Lys Ser Thr Gly Lys Ser His Ser Val Lys His Leu Gln
 65 70 75 80

Phe Ile Lys Trp Pro Asp His Gly Thr Pro Ala Ser Val Asp Phe Phe
 85 90 95

Ile Lys Tyr Val Arg Tyr Val Arg Lys Ser His Ile Thr Gly Pro Leu
 100 105 110

Leu Val His Cys Thr Ala Gly Val Gly Arg
 115 120

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: The letter "Y" stands for C or T.

The letter "V" stands for A, C or G.
 The letter "R" stands for A or G.
 The letter "N" stands for A, C, G or T.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAYTTYTGGV RNATGRTNTG GGA

23

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: The letter "S" stands for C or G.
 The letter "Y" stands for C or T.
 The letter "N" stands for A, C, G or T.
 The letter "W" stands for A or T.
 The letter "R" stands for A or G.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGGCCSAYNC CNGCNSWRCA RTG

23

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: "Xaa" in positions 4 and 6 stand for an unspecified amino acid.
 "Xaa" in position 8 stands for either Glu or Asp.

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Asp Phe Trp Xaa Met Xaa Trp Xaa
 1 5

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(D) OTHER INFORMATION: "Xaa" in positions 3 and 6 stand for an unspecified amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

His Cys Xaa Ala Gly Xaa Gly
1 5

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CACCGTTCGA GTATTCAGA TTGTGAAGAA GTCC

34

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGACTTCTTC ACAATCTGAA ATACTCGAAC GGTG

34

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCGTTATGTG AGGAAGAGCC ACATTACAGG ACC

33

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGTCCTGTAA TGTGGCTCTT CCTCACATAA CGG

33

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CACCGTTCGA GTATTCAGA TTGTGAAGAA GTCC

34

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGTCCTGTAA TGTGGCTCTT CCTCACATAA CGG

33

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

His Cys Ser Ala Gly
1 5

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Ser Ser Pro Arg Lys Val Arg Gly Lys Thr Gly Arg Asp Asn Asp
1 5 10 15

Glu Glu Glu Gly Asn Ser Gly Asn Leu Asn Leu Arg Asn
20 25

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ser Pro Val Leu Ser Gly Ser Ser Arg Leu Ser Lys Asp Thr Glu Thr
1 5 10 15

Ser Val Ser Glu Lys Glu Leu Thr Gln Leu Ala Gln Ile
20 25

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Trp Asp Val Ser Asp Arg Ser Leu Arg Asn Arg Trp Asn Ser Met Asp
1 5 10 15

Ser Glu Thr Ala Gly Pro Ser Lys Thr Val Ser Pro Val
20 25